

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Koji YANAI et al.
- (ii) TITLE OF INVENTION: β -FRUCTOFURANOSIDASE AND ITS GENE,
METHOD OF ISOLATING β -FRUCTOFURANOSIDASE GENE, SYSTEM
FOR PRODUCING β -FRUCTOFURANOSIDASE, AND
 β -FRUCTOFURANOSIDASE VARIANT
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 - (B) STREET: 2033 K Street, N.W., Suite 800
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20006
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: MS-DOS
 - (D) SOFTWARE: Wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: NEW
 - (B) FILING DATE: November 23, 2001
- (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/142,623

(B) FILING DATE: September 10, 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lee Cheng

(B) REGISTRATION NUMBER: 40,949

(C) REFERENCE/DOCKET NUMBER: 2001-1611

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-721-8200

(B) TELEFAX: 202-721-8250

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acid residues

(B) TYPE: amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1

(ATCC 20611)

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1..635

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Tyr His Leu Asp Thr Thr Ala Pro Pro Pro Thr Asn Leu Ser Thr
1 5 10 15
Leu Pro Asn Asn Thr Leu Phe His Val Trp Arg Pro Arg Ala His Ile
20 25 30
Leu Pro Ala Glu Gly Gln Ile Gly Asp Pro Cys Ala His Tyr Thr Asp
35 40 45
Pro Ser Thr Gly Leu Phe His Val Gly Phe Leu His Asp Gly Asp Gly
50 55 60
Ile Ala Gly Ala Thr Thr Ala Asn Leu Ala Thr Tyr Thr Asp Thr Ser
65 70 75 80
Asp Asn Gly Ser Phe Leu Ile Gln Pro Gly Gly Lys Asn Asp Pro Val
85 90 95
Ala Val Phe Asp Gly Ala Val Ile Pro Val Gly Val Asn Asn Thr Pro
100 105 110
Thr Leu Leu Tyr Thr Ser Val Ser Phe Leu Pro Ile His Trp Ser Ile
115 120 125
Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ala Arg Asp
130 135 140
Gly Gly Arg Arg Phe Asp Lys Leu Asp Gln Gly Pro Val Ile Ala Asp
145 150 155 160
His Pro Phe Ala Val Asp Val Thr Ala Phe Arg Asp Pro Phe Val Phe
165 170 175
Arg Ser Ala Lys Leu Asp Val Leu Leu Ser Leu Asp Glu Glu Val Ala
180 185 190

Arg	Asn	Glu	Thr	Ala	Val	Gln	Gln	Ala	Val	Asp	Gly	Trp	Thr	Glu	Lys
	195						200					205			
Asn	Ala	Pro	Trp	Tyr	Val	Ala	Val	Ser	Gly	Gly	Val	His	Gly	Val	Gly
	210						215					220			
Pro	Ala	Gln	Phe	Leu	Tyr	Arg	Gln	Asn	Gly	Gly	Asn	Ala	Ser	Glu	Phe
	225					230					235			240	
Gln	Tyr	Trp	Glu	Tyr	Leu	Gly	Glu	Trp	Trp	Gln	Glu	Ala	Thr	Asn	Ser
					245					250				255	
Ser	Trp	Gly	Asp	Glu	Gly	Thr	Trp	Ala	Gly	Arg	Trp	Gly	Phe	Asn	Phe
				260					265					270	
Glu	Thr	Gly	Asn	Val	Leu	Phe	Leu	Thr	Glu	Glu	Gly	His	Asp	Pro	Gln
		275						280					285		
Thr	Gly	Glu	Val	Phe	Val	Thr	Leu	Gly	Thr	Glu	Gly	Ser	Gly	Leu	Pro
	290						295					300			
Ile	Val	Pro	Gln	Val	Ser	Ser	Ile	His	Asp	Met	Leu	Trp	Ala	Ala	Gly
	305					310					315			320	
Glu	Val	Gly	Val	Gly	Ser	Glu	Gln	Glu	Gly	Ala	Lys	Val	Glu	Phe	Ser
						325				330				335	
Pro	Ser	Met	Ala	Gly	Phe	Leu	Asp	Trp	Gly	Phe	Ser	Ala	Tyr	Ala	Ala
			340						345					350	
Ala	Gly	Lys	Val	Leu	Pro	Ala	Ser	Ser	Ala	Val	Ser	Lys	Thr	Ser	Gly
		355						360					365		
Val	Glu	Val	Asp	Arg	Tyr	Val	Ser	Phe	Val	Trp	Leu	Thr	Gly	Asp	Gln
	370							375					380		

Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly Trp Thr Gly
 385 390 395 400
 Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val Glu Asn Val
 405 410 415
 Val Asp Asn Glu Leu Val Arg Glu Glu Gly Val Ser Trp Val Val Gly
 420 425 430
 Glu Ser Asp Asn Gln Thr Ala Arg Leu Arg Thr Leu Gly Ile Thr Ile
 435 440 445
 Ala Arg Glu Thr Lys Ala Ala Leu Leu Ala Asn Gly Ser Val Thr Ala
 450 455 460
 Glu Glu Asp Arg Thr Leu Gln Thr Ala Ala Val Val Pro Phe Ala Gln
 465 470 475 480
 Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Gln Leu Glu Phe Pro
 485 490 495
 Ala Ser Ala Arg Ser Ser Pro Leu Gln Ser Gly Phe Glu Ile Leu Ala
 500 505 510
 Ser Glu Leu Glu Arg Thr Ala Ile Tyr Tyr Gln Phe Ser Asn Glu Ser
 515 520 525
 Leu Val Val Asp Arg Ser Gln Thr Ser Ala Ala Ala Pro Thr Asn Pro
 530 535 540
 Gly Leu Asp Ser Phe Thr Glu Ser Gly Lys Leu Arg Leu Phe Asp Val
 545 550 555 560
 Ile Glu Asn Gly Gln Glu Gln Val Glu Thr Leu Asp Leu Thr Val Val
 565 570 575

Val Asp Asn Ala Val Val Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu		
580	585	590
Ser Thr Trp Ala Arg Ser Trp Tyr Asp Asn Ser Thr Gln Ile Arg Phe		
595	600	605
Phe His Asn Gly Glu Gly Glu Val Gln Phe Arg Asn Val Ser Val Ser		
610	615	620
Glu Gly Leu Tyr Asn Ala Trp Pro Glu Arg Asn		
625	630	635

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1 .. 1905
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCATACCACC	TGGACACCAC	GGCCCCGCCG	CCGACCAACC	TCAGCACCCCT	CCCCAACAAAC	60
ACCCTCTTCC	ACGTGTGGCG	GCCGCGCGCG	CACATCCTGC	CCGCCGAGGG	CCAGATCGGC	120
GACCCCTGCG	CGCACTACAC	CGACCCATCC	ACCGGCCTCT	TCCACGTGGG	GTTCTGTCAC	180
GACGGGGACG	GCATCGCGGG	CGCCACCACG	GCCAACCTGG	CCACCTACAC	CGATACCTCC	240
GATAACGGGA	GCTTCCTGAT	CCAGCCGGGC	GGGAAGAACG	ACCCCGTCGC	CGTGTTTCGAC	300
GGCGCCGTCA	TCCCCGTCGG	CGTCAACAAC	ACCCCCACCT	TACTCTACAC	CTCCGTCTCC	360
TTCTGCCCA	TCCACTGGTC	CATCCCCTAC	ACCCGCGGCA	GCGAGACGCA	GTCGTTGGCC	420
GTCGCGCGCG	ACGGCGGGCCG	CCGCTTCGAC	AAGCTCGACC	AGGGCCCCGT	CATCGCCGAC	480
CACCCCTTCG	CCGTCGACGT	CACCGCCTTC	CGCGATCCGT	TTGTCTTCCG	CAGTGCCAAG	540
TTGGATGTGC	TGCTGTCTGT	GGATGAGGAG	GTGGCGCGGA	ATGAGACGGC	CGTGCAGCAG	600
GCCGTTCGATG	GCTGGACCGA	GAAGAACGCC	CCCTGGTATG	TCGCGGTCTC	TGGCGGGGTG	660
CACGGCGTCG	GGCCCGCGCA	GTTCTCTAC	CGCCAGAACG	GCGGGAACGC	TTCCGAGTTC	720
CAGTACTGGG	AGTACCTCGG	GGAGTGGTGG	CAGGAGGCGA	CCAACTCCAG	CTGGGGCGAC	780
GAGGGCACCT	GGGCCGGGCG	CTGGGGGTTC	AACTTCGAGA	CGGGGAATGT	GCTCTTCCTC	840
ACCGAGGAGG	GCCATGACCC	CCAGACGGGC	GAGGTGTTTCG	TCACCCTCGG	CACGGAGGGG	900
TCTGGCCTGC	CAATCGTGCC	GCAGGTCTCC	AGTATCCACG	ATATGCTGTG	GGCGGCGGGT	960
GAGGTGCGGG	TGGGCAGTGA	GCAGGAGGGT	GCCAAGGTCG	AGTTCTCCCC	CTCCATGGCC	1020
GGGTTTCTGG	ACTGGGGGTT	CAGCGCCTAC	GCTGCGGCGG	GCAAGGTGCT	GCCGGCCAGC	1080
TCGGCGGTGT	CGAAGACCAG	CGGCGTGGAG	GTGGATCGGT	ATGTCTCGTT	CGTCTGGTTG	1140
ACGGGCGACC	AGTACGAGCA	GGCGGACGGG	TTCCCCACGG	CCCAGCAGGG	GTGGACGGGG	1200
TCGCTGCTGC	TGCCGCGCGA	GCTGAAGGTG	CAGACGGTGG	AGAACGTTCGT	CGACAACGAG	1260
CTGGTGCGCG	AGGAGGGCGT	GTCGTGGGTG	GTGGGGGAGT	CGGACAACCA	GACGGCCAGG	1320
CTGCGCACGC	TGGGGATCAC	GATCGCCCGG	GAGACCAAGG	CGGCCCTGCT	GGCCAACGGC	1380
TCGGTGACCG	CGGAGGAGGA	CCGCACGCTG	CAGACGGCGG	CCGTCTGTCC	GTTTCGCGCAA	1440
TCGCCGAGCT	CCAAGTTCTT	CGTGCTGACG	GCCCAGCTGG	AGTTCCCCGC	GAGCGCGCGC	1500

TCGTCCCCGC TCCAGTCCGG GTTCGAAATC CTGGCGTCGG AGCTGGAGCG CACGGCCATC 1560
TACTACCAGT TCAGCAACGA GTCGCTGGTC GTCGACCGCA GCCAGACTAG TGCGGCGGCG 1620
CCCACGAACC CCGGGCTGGA TAGCTTTACT GAGTCCGGCA AGTTGCGGTT GTTCGACGTG 1680
ATCGAGAACG GCCAGGAGCA GGTTCGAGACG TTGGATCTCA CTGTCGTCGT GGATAACGCG 1740
GTTGTCGAGG TGTATGCCAA CGGGCGCTTT GCGTTGAGCA CCTGGGCGAG ATCGTGGTAC 1800
GACAACTCCA CCCAGATCCG CTTCTTCCAC AACGGCGAGG GCGAGGTGCA GTTCAGGAAT 1860
GTCTCCGTGT CGGAGGGGCT CTATAACGCC TGGCCGGAGA GAAAT 1905

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Asp Gln Gly Pro Val Ile Ala Asp His Pro Phe Ala Val Asp Val
1 5 10 15
Thr Ala Phe Arg
20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1

(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Glu Phe Ser Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser
1 5 10 15
Ala Tyr Ala Ala
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Gln Thr Val Glu Asn Val Val Asp Asn Glu Leu Val Arg Glu Glu
1 5 10 15
Gly Val Ser Trp
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acid residues
(B) TYPE: Amino acid
(C) STRANDEDNESS: Not relevant
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Ala Leu Leu Ala Xaa Gly Ser Val Thr Ala Glu Glu Asp Arg Thr
1 5 10 15
Leu Gln Thr Ala
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Tyr His Leu Asp Thr

1

5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATCGCSGAYC AYCCSTTYGC 20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCRTTRTCSA CSACRTTYTC 20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(ix) FEATURE:

- (A) NAME/KEY: P CDS(partial amino acid sequence)
- (B) LOCATION: 1 .. 788
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATC GCC GAC CAC CCC TTC GCC GTC GAC GTC ACC GCC TTC CGC GAT CCG	48
Ile Ala Asp His Pro Phe Ala Val Asp Val Thr Ala Phe Arg Asp Pro	
1 5 10 15	
TTT GTC TTC CGC AGT GCC AAG TTG GAT GTG CTG CTG TCG TTG GAT GAG	96
Phe Val Phe Arg Ser Ala Lys Leu Asp Val Leu Leu Ser Leu Asp Glu	
20 25 30	
GAG GTG GCG CGG AAT GAG ACG GCC GTG CAG CAG GCC GTC GAT GGC TGG	144
Glu Val Ala Arg Asn Glu Thr Ala Val Gln Gln Ala Val Asp Gly Trp	
35 40 45	
ACC GAG AAG AAC GCC CCC TGG TAT GTC GCG GTC TCT GGC GGG GTG CAC	192
Thr Glu Lys Asn Ala Pro Trp Tyr Val Ala Val Ser Gly Gly Val His	
50 55 60	
GGC GTC GGG CCC GCG CAG TTC CTC TAC CGC CAG AAC GGC GGG AAC GCT	240
Gly Val Gly Pro Ala Gln Phe Leu Tyr Arg Gln Asn Gly Gly Asn Ala	
65 70 75 80	
TCC GAG TTC CAG TAC TGG GAG TAC CTC GGG GAG TGG TGG CAG GAG GCG	288
Ser Glu Phe Gln Tyr Trp Glu Tyr Leu Gly Glu Trp Trp Gln Glu Ala	
85 90 95	
ACC AAC TCC AGC TGG GGC GAC GAG GGC ACC TGG GCC GGG CGC TGG GGG	336
Thr Asn Ser Ser Trp Gly Asp Glu Gly Thr Trp Ala Gly Arg Trp Gly	
100 105 110	
TTC AAC TTC GAG ACG GGG AAT GTG CTC TTC CTC ACC GAG GAG GGC CAT	384
Phe Asn Phe Glu Thr Gly Asn Val Leu Phe Leu Thr Glu Glu Gly His	
115 120 125	

GAC CCC CAG ACG GGC GAG GTG TTC GTC ACC CTC GGC ACG GAG GGG TCT	432
Asp Pro Gln Thr Gly Glu Val Phe Val Thr Leu Gly Thr Glu Gly Ser	
130 135 140	
GGC CTG CCA ATC GTG CCG CAG GTC TCC AGT ATC CAC GAT ATG CTG TGG	480
Gly Leu Pro Ile Val Pro Gln Val Ser Ser Ile His Asp Met Leu Trp	
145 150 155 160	
GCG GCG GGT GAG GTC GGG GTG GGC AGT GAG CAG GAG GGT GCC AAG GTC	528
Ala Ala Gly Glu Val Gly Val Gly Ser Glu Gln Glu Gly Ala Lys Val	
165 170 175	
GAG TTC TCC CCC TCC ATG GCC GGG TTT CTG GAC TGG GGG TTC AGC GCC	576
Glu Phe Ser Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser Ala	
180 185 190	
TAC GCT GCG GCG GGC AAG GTG CTG CCG GCC AGC TCG GCG GTG TCG AAG	624
Tyr Ala Ala Ala Gly Lys Val Leu Pro Ala Ser Ser Ala Val Ser Lys	
195 200 205	
ACC AGC GGC GTG GAG GTG GAT CGG TAT GTC TCG TTC GTC TGG TTG ACG	672
Thr Ser Gly Val Glu Val Asp Arg Tyr Val Ser Phe Val Trp Leu Thr	
210 215 220	
GGC GAC CAG TAC GAG CAG GCG GAC GGG TTC CCC ACG GCC CAG CAG GGG	720
Gly Asp Gln Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly	
225 230 235 240	
TGG ACG GGG TCG CTG CTG CTG CCG CGC GAG CTG AAG GTG CAG ACG GTG	768
Trp Thr Gly Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val	
245 250 255	

GAG AAC GTC GTC GAC AAC GA

Glu Asn Val Val Asp Asn

260

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565 amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Penicillium roqueforti* IAM7254

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1 .. 565

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val	Asp	Phe	His	Thr	Pro	Ile	Asp	Tyr	Asn	Ser	Ala	Pro	Pro	Asn	Leu
1				5					10					15	
Ser	Thr	Leu	Ala	Asn	Ala	Ser	Leu	Phe	Lys	Thr	Trp	Arg	Pro	Arg	Ala
			20					25					30		
His	Leu	Leu	Pro	Pro	Ser	Gly	Asn	Ile	Gly	Asp	Pro	Cys	Gly	His	Tyr
			35					40					45		

Thr Asp Pro Lys Thr Gly Leu Phe His Val Gly Trp Leu Tyr Ser Gly
 50 55 60
 Ile Ser Gly Ala Thr Thr Asp Asp Leu Val Thr Tyr Lys Asp Leu Asn
 65 70 75 80
 Pro Asp Gly Ala Pro Ser Ile Val Ala Gly Gly Lys Asn Asp Pro Leu
 85 90 95
 Ser Val Phe Asp Gly Ser Val Ile Pro Ser Gly Ile Asp Gly Met Pro
 100 105 110
 Thr Leu Leu Tyr Thr Ser Val Ser Tyr Leu Pro Ile His Trp Ser Ile
 115 120 125
 Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ser Tyr Asp
 130 135 140
 Gly Gly His Asn Phe Thr Lys Leu Asn Gln Gly Pro Val Ile Pro Thr
 145 150 155 160
 Pro Pro Phe Ala Leu Asn Val Thr Ala Phe Arg Asp Pro Tyr Val Phe
 165 170 175
 Gln Ser Pro Ile Leu Asp Lys Ser Val Asn Ser Thr Gln Gly Thr Trp
 180 185 190
 Tyr Val Ala Ile Ser Gly Gly Val His Gly Val Gly Pro Cys Gln Phe
 195 200 205
 Leu Tyr Arg Gln Asn Asp Ala Asp Phe Gln Tyr Trp Glu Tyr Leu Gly
 210 215 220
 Gln Trp Trp Lys Glu Pro Leu Asn Thr Thr Trp Gly Lys Gly Asp Trp
 225 230 235 240

Ala Gly Gly Trp Gly Phe Asn Phe Glu Val Gly Asn Val Phe Ser Leu

245 250 255

Asn Ala Glu Gly Tyr Ser Glu Asp Gly Glu Ile Phe Ile Thr Leu Gly

260 265 270

Ala Glu Gly Ser Gly Leu Pro Ile Val Pro Gln Val Ser Ser Ile Arg

275 280 285

Asp Met Leu Trp Val Thr Gly Asn Val Thr Asn Asp Gly Ser Val Thr

290 295 300

Phe Lys Pro Thr Met Ala Gly Val Leu Asp Trp Gly Val Ser Ala Tyr

305 310 315 320

Ala Ala Ala Gly Lys Ile Leu Pro Ala Ser Ser Gln Ala Ser Thr Lys

325 330 335

Ser Gly Ala Pro Asp Arg Phe Ile Ser Tyr Val Trp Leu Thr Gly Asp

340 345 350

Leu Phe Glu Gln Val Lys Gly Phe Pro Thr Ala Gln Gln Asn Trp Thr

355 360 365

Gly Ala Leu Leu Leu Pro Arg Glu Leu Asn Val Arg Thr Ile Ser Asn

370 375 380

Val Val Asp Asn Glu Leu Ser Arg Glu Ser Leu Thr Ser Trp Arg Val

385 390 395 400

Ala Arg Glu Asp Ser Gly Gln Ile Asp Leu Glu Thr Met Gly Ile Ser

405 410 415

Ile Ser Arg Glu Thr Tyr Ser Ala Leu Thr Ser Gly Ser Ser Phe Val

420 425 430

Glu Ser Gly Lys Thr Leu Ser Asn Ala Gly Ala Val Pro Phe Asn Thr
 435 440 445
 Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Asn Ile Ser Phe Pro
 450 455 460
 Thr Ser Ala Arg Asp Ser Gly Ile Gln Ala Gly Phe Gln Val Leu Ser
 465 470 475 480
 Ser Ser Leu Glu Ser Thr Thr Ile Tyr Tyr Gln Phe Ser Asn Glu Ser
 485 490 495
 Ile Ile Val Asp Arg Ser Asn Thr Ser Ala Ala Ala Arg Thr Thr Ala
 500 505 510
 Gly Ile Leu Ser Asp Asn Glu Ala Gly Arg Leu Arg Leu Phe Asp Val
 515 520 525
 Leu Arg Asn Gly Lys Glu Gln Val Glu Thr Leu Glu Leu Thr Ile Val
 530 535 540
 Val Asp Asn Ser Val Leu Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu
 545 550 555 560
 Gly Thr Trp Ala Arg
 565

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1695 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Penicillium roqueforti* IAM7254

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1 .. 1695

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGATTTC	ATACCCCGAT	TGACTATAAC	TCGGCTCCGC	CAAACCTTTC	TACCCTGGCA	60
AACGCATCTC	TTTTCAAGAC	ATGGAGACCC	AGAGCCCATC	TTCTCCCTCC	ATCTGGGAAC	120
ATAGGCGACC	CGTGCGGGCA	CTATACCGAT	CCCAAGACTG	GTCTCTTCCA	CGTGGGTTGG	180
CTTTACAGTG	GGATTTTCGGG	AGCGACAACC	GACGATCTCG	TTACCTATAA	AGACCTCAAT	240
CCCGATGGAG	CCCCGTCAAT	TGTTGCAGGA	GGAAAGAACG	ACCCTCTTTC	TGTCTTCGAT	300
GGCTCGGTCA	TTCCAAGCGG	TATAGACGGC	ATGCCAACTC	TTCTGTATAC	CTCTGTATCA	360
TACCTCCCAA	TCCACTGGTC	CATCCCCTAC	ACCCGGGGAA	GCGAGACACA	ATCCTTGGCC	420
GTTTCCTATG	ACGGTGGTCA	CAACTTCACC	AAGCTCAACC	AAGGGCCCGT	GATCCCTACG	480
CCTCCGTTTG	CTCTCAATGT	CACCGCTTTC	CGTGACCCCT	ACGTTTTC	CA AAGCCCAATT	540
CTGGACAAAT	CTGTCAATAG	TACCCAAGGA	ACATGGTATG	TCGCCATATC	TGGCGGTGTC	600
CACGGTGTCTG	GACCTTGTC	GTTCTCTAC	CGTCAGAACG	ACGCAGATTT	TCAATATTGG	660
GAATATCTCG	GGCAATGGTG	GAAGGAGCCC	CTTAATACCA	CTTGGGGAAA	GGGTGACTGG	720
GCCGGGGGTT	GGGGCTTCAA	CTTTGAGGTT	GGCAACGTCT	TTAGTCTGAA	TGCAGAGGGG	780
TATAGTGAAG	ACGGCGAGAT	ATTCATAACC	CTCGGTGCTG	AGGGTTCGGG	ACTTCCCATC	840
GTTCTCAAG	TCTCCTCTAT	TCGCGATATG	CTGTGGGTGA	CCGGCAATGT	CACAAATGAC	900
GGCTCTGTCA	CTTTCAAGCC	AACCATGGCG	GGTGTGCTTG	ACTGGGGCGT	GTCGGCATAT	960
GCTGCTGCAG	GCAAGATCTT	GCCGGCCAGC	TCTCAGGCAT	CCACAAAGAG	CGGTGCCCCC	1020

GATCGGTTCA	TTTCCTATGT	CTGGCTCACT	GGAGATCTAT	TCGAGCAAGT	GAAAGGATTC	1080
CCTACCGCTC	AACAAAACGT	GACCGGGGCC	CTCTTACTGC	CGCGAGAGCT	GAATGTCCGC	1140
ACTATCTCTA	ACGTGGTGGA	TAACGAACTT	TCGCGTGAGT	CCTTGACATC	GTGGCGCGTG	1200
GCCCCGGAAG	ACTCTGGTCA	GATCGACCTT	GAAACAATGG	GAATCTCAAT	TTCCAGGGAG	1260
ACTTACAGCG	CTCTCACATC	CGGCTCATCT	TTTGTGAGT	CTGGTAAAAC	GTTGTCGAAT	1320
GCTGGAGCAG	TGCCCTTCAA	TACCTACCC	TCAAGCAAGT	TCTTCGTGCT	GACAGCAAAT	1380
ATATCTTTCC	CGACCTCTGC	CCGTGACTCT	GGCATCCAGG	CTGGTTTCCA	GGTTTTATCC	1440
TCTAGTCTTG	AGTCTACAAC	TATCTACTAC	CAATTCTCCA	ACGAGTCCAT	CATCGTCGAC	1500
CGCAGCAACA	CGAGTGCTGC	GGCGAGAACA	ACTGCTGGGA	TCCTCAGTGA	TAACGAGGCG	1560
GGACGTCTGC	GCCTCTTCGA	CGTGTTGCGA	AATGGAAAAG	AACAGGTTGA	AACTTTGGAG	1620
CTCACTATCG	TGGTGGATAA	TAGTGACTG	GAAGTATATG	CCAATGGACG	CTTTGCTCTA	1680
GGCACTTGGG	CTCGG					1695

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Scopulariopsis brevicaulis* IF04843

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1 .. 574

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Pro Thr Ser Leu Ser Ile Asp Asn Ser Thr Tyr Pro Ser Ile Asp
1 5 10 15
Tyr Asn Ser Ala Pro Pro Asn Leu Ser Thr Leu Ala Asn Asn Ser Leu
20 25 30
Phe Glu Thr Trp Arg Pro Arg Ala His Val Leu Pro Pro Gln Asn Gln
35 40 45
Ile Gly Asp Pro Cys Met His Tyr Thr Asp Pro Glu Thr Gly Ile Phe
50 55 60
His Val Gly Trp Leu Tyr Asn Gly Asn Gly Ala Ser Gly Ala Thr Thr
65 70 75 80
Glu Asp Leu Val Thr Tyr Gln Asp Leu Asn Pro Asp Gly Ala Gln Met
85 90 95
Ile Leu Pro Gly Gly Val Asn Asp Pro Ile Ala Val Phe Asp Gly Ala
100 105 110
Val Ile Pro Ser Gly Ile Asp Gly Lys Pro Thr Met Met Tyr Thr Ser
115 120 125
Val Ser Tyr Met Pro Ile Ser Trp Ser Ile Ala Tyr Thr Arg Gly Ser
130 135 140
Glu Thr His Ser Leu Ala Val Ser Ser Asp Gly Gly Lys Asn Phe Thr
145 150 155 160
Lys Leu Val Gln Gly Pro Val Ile Pro Ser Pro Pro Phe Gly Ala Asn
165 170 175

Val Thr Ser Trp Arg Asp Pro Phe Leu Phe Gln Asn Pro Gln Phe Asp
 180 185 190
 Ser Leu Leu Glu Ser Glu Asn Gly Thr Trp Tyr Thr Val Ile Ser Gly
 195 200 205
 Gly Ile His Gly Asp Gly Pro Ser Ala Phe Leu Tyr Arg Gln His Asp
 210 215 220
 Pro Asp Phe Gln Tyr Trp Glu Tyr Leu Gly Pro Trp Trp Asn Glu Glu
 225 230 235 240
 Gly Asn Ser Thr Trp Gly Ser Gly Asp Trp Ala Gly Arg Trp Gly Tyr
 245 250 255
 Asn Phe Glu Val Ile Asn Ile Val Gly Leu Asp Asp Asp Gly Tyr Asn
 260 265 270
 Pro Asp Gly Glu Ile Phe Ala Thr Val Gly Thr Glu Trp Ser Phe Asp
 275 280 285
 Pro Ile Lys Pro Gln Ala Ser Asp Asn Arg Glu Met Leu Trp Ala Ala
 290 295 300
 Gly Asn Met Thr Leu Glu Asp Gly Asp Ile Lys Phe Thr Pro Ser Met
 305 310 315 320
 Ala Gly Tyr Leu Asp Trp Gly Leu Ser Ala Tyr Ala Ala Ala Gly Lys
 325 330 335
 Glu Leu Pro Ala Ser Ser Lys Pro Ser Gln Lys Ser Gly Ala Pro Asp
 340 345 350
 Arg Phe Val Ser Tyr Leu Trp Leu Thr Gly Asp Tyr Phe Glu Gly His
 355 360 365

Asp	Phe	Pro	Thr	Pro	Gln	Gln	Asn	Trp	Thr	Gly	Ser	Leu	Leu	Leu	Pro
370							375				380				
Arg	Glu	Leu	Ser	Val	Gly	Thr	Ile	Pro	Asn	Val	Val	Asp	Asn	Glu	Leu
385					390					395				400	
Ala	Arg	Glu	Thr	Gly	Ser	Trp	Arg	Val	Gly	Thr	Asn	Asp	Thr	Gly	Val
				405					410					415	
Leu	Glu	Leu	Val	Thr	Leu	Lys	Gln	Glu	Ile	Ala	Arg	Glu	Thr	Leu	Ala
			420					425						430	
Glu	Met	Thr	Ser	Gly	Asn	Ser	Phe	Thr	Glu	Ala	Ser	Arg	Asn	Val	Ser
			435				440					445			
Ser	Pro	Gly	Ser	Thr	Ala	Phe	Gln	Gln	Ser	Leu	Asp	Ser	Lys	Phe	Phe
		450				455					460				
Val	Leu	Thr	Ala	Ser	Leu	Ser	Phe	Pro	Ser	Ser	Ala	Arg	Asp	Ser	Asp
465					470					475				480	
Leu	Lys	Ala	Gly	Phe	Glu	Ile	Leu	Ser	Ser	Glu	Phe	Glu	Ser	Thr	Thr
				485					490					495	
Val	Tyr	Tyr	Gln	Phe	Ser	Asn	Glu	Ser	Ile	Ile	Ile	Asp	Arg	Ser	Asn
			500					505					510		
Ser	Ser	Ala	Ala	Ala	Leu	Thr	Thr	Asp	Gly	Ile	Asp	Thr	Arg	Asn	Glu
		515					520					525			
Phe	Gly	Lys	Met	Arg	Leu	Phe	Asp	Val	Val	Glu	Gly	Asp	Gln	Glu	Arg
		530				535						540			
Ile	Glu	Thr	Leu	Asp	Leu	Thr	Ile	Val	Val	Asp	Asn	Ser	Ile	Val	Glu
545					550					555				560	

Val His Ala Asn Gly Arg Phe Ala Leu Ser Thr Trp Val Arg

565

570

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1722 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double stranded

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Scopulariopsis brevicaulis* IFO4843

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1 .. 1722

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAACCTACGT CTCTGTCAAT CGACAATTCC ACGTATCCTT CTATCGACTA CAACTCCGCC	60
CCTCCAAACC TCTCGACTCT TGCCAACAAC AGCCTCTTCG AGACATGGAG GCCGAGGGCA	120
CACGTCCTTC CGCCCCAGAA CCAGATCGGC GATCCGTGTA TGCACTACAC CGACCCCGAG	180
ACAGGAATCT TCCACGTCGG CTGGCTGTAC AACGGCAATG GCGCTTCCGG CGCCACGACC	240
GAGGATCTCG TCACCTATCA GGATCTCAAC CCCGACGGAG CGCAGATGAT CCTTCCGGGT	300
GGTGTGAATG ACCCCATTGC TGTCTTTGAC GGCGCGGTAA TTCCCAGTGG CATTGATGGG	360
AAACCCACCA TGATGTATAC CTCGGTGTCA TACATGCCCA TCTCCTGGAG CATCGCTTAC	420
ACCAGGGGAA GCGAGACCCA CTCTCTCGCA GTGTCTGTCG ACGGCGGTAA GAACTTCACC	480

AAGCTGGTGC	AGGGCCCCGT	CATTCCTTCG	CCTCCCTTCG	GCGCCAACGT	GACCAGCTGG	540
CGTGACCCCT	TCCTGTTCCA	AAACCCCCAG	TTGACTCTC	TCCTCGAAAG	CGAGAACGGC	600
ACGTGGTACA	CCGTTATCTC	TGGTGGCATC	CACGGTGACG	GCCCCCTCCG	GTTCCCTCTAC	660
CGTCAGCACG	ACCCCGACTT	CCAGTACTGG	GAGTACCTTG	GACCGTGGTG	GAACGAGGAA	720
GGGAACTCGA	CCTGGGGCAG	CGGTGACTGG	GCTGGCCGGT	GGGGCTACAA	CTTCGAGGTC	780
ATCAACATTG	TCGGTCTTGA	CGATGATGGC	TACAACCCCG	ACGGTGAAAT	CTTTGCCACG	840
GTAGGTACCG	AATGGTCGTT	TGACCCCATC	AAACCGCAGG	CCTCGGACAA	CAGGGAGATG	900
CTCTGGGCCG	CGGGCAACAT	GACTCTCGAG	GACGGCGATA	TCAAGTTCAC	GCCAAGCATG	960
GCGGGCTACC	TCGACTGGGG	TCTATCGGCG	TATGCCGCCG	CTGGCAAGGA	GCTGCCCCGCT	1020
TCTTCAAAGC	CTTCGCAGAA	GAGCGGTGCG	CCGGACCGGT	TCGTGTCGTA	CCTGTGGGCTC	1080
ACCGGTGACT	ACTTCGAGGG	CCACGACTTC	CCCACCCCGC	AGCAGAATTG	GACCGGCTCG	1140
CTTTTGCTTC	CGCGTGAGCT	GAGCGTCGGG	ACGATTCCCA	ACGTTGTCGA	CAACGAGCTT	1200
GCTCGCGAGA	CGGGCTCTTG	GAGGGTTGGC	ACCAACGACA	CTGGCGTGCT	TGAGCTGGTC	1260
ACTCTGAAGC	AGGAGATTGC	TCGCGAGACG	CTGGCTGAAA	TGACCAGCGG	CAACTCCTTC	1320
ACCGAGGCGA	GCAGGAATGT	CAGCTCGCCC	GGATCTACCG	CCTTCCAGCA	GTCCCTGGAT	1380
TCCAAGTTCT	TCGTCTTGAC	CGCCTCGCTC	TCCTTCCCTT	CGTCGGCTCG	CRACTCCGAC	1440
CTCAAGGCTG	GTTTCGAGAT	CCTGTCTGCC	GAGTTTGAGT	CGACCACGGT	CTACTACCAG	1500
TTTTCCAACG	AGTCCATCAT	CATTGACCGG	AGCAACTCGA	GTGCTGCCGC	CTTGACTACC	1560
GATGGAATCG	ACACCCGCAA	CGAGTTTGGC	AAGATGCGCC	TGTTTGATGT	TGTCGAGGGT	1620
GACCAGGAGC	GTATCGAGAC	GCTCGATCTC	ACTATTGTGG	TTGATAACTC	GATCGTTGAG	1680
GTTCATGCCA	ACGGGCGATT	CGCTCTGAGC	ACTTGGGTTC	GG		1722

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGAATTCCA ATGAAGCTCA CCACTACC

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGGATCCCG GTCAATTTCT CTCC

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTGACCGG TGTCATCC

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCGGTTGTC ATAGATGTGG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAATCCAGGA GGATCCCAAT GAAG

24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

81

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGACCGGGAT CCGGGCATGC AG

22

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGTCGTCT AGAGGTTGTC ACTT

24

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCTATTGGG GTCCATGGCC C

21

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAACTGCTGG CATCCTCAGT GA

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGGATCCAT GAAGCTATCA AATGCAATCA

30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

83

- (A) LENGTH: 26 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCGGATCCTT ACCGAGCCCA AGTGCC

26

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGGATCCAA TGAAGCTCAC CACTACC

27

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCGGATCCCG GTCAATTTCT CTCC

24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCACCGCCT GCGCGATCC G

21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCACGGAGT GGTCTGGCC

19

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTCCAGTATC AAGGATATGC TGTG

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGACCAGTAC AAGCAGGCGG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCCAGTATCC GCGATATGCT G

21

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGCACGGAG GTTTCTGGCC TGC

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGGCACGGAG GAGTCTGGCC TGC

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGGCACGGAG GATTCTGGCC TGC

23

CGGCACGGAG GATTCTGGCC TGC